# METHOD FOR THE QUANTITATIVE DETECTION OF NUCLEIC ACIDS

The present invention relates to a method for quantitative detection of nucleic acids from a biological fluid sample.

The method of the invention may be suitably applied to diagnosis of viral and any other pathogenic agents and to monitor safety and/or genetic

5   composition of waters, foods and plant species used in the alimentary field.

## BACKGROUND ART

A commonly used strategy to detect the presence of pathogens, in biological fluids, is the detection of an antigen (direct method) or a

10   respective antibody (indirect method). However, this strategy, performed with immunometric techniques such as ELISA, IFA or Western Blotting, is limited because of the scarce quantitation accuracy, precision and sensitivity, of the different antibody cross-reactivity and of the impossibility to obtain precocious diagnosis.

15   Another approach relies on the detection of nucleic acids specific for each kind of molecular target from any biological source, using the amplification by polymerase chain reaction (PCR). This technique, in its more sophisticated version i.e. the quantitative competitive PCR (qcPCR), makes it possible to reach a high sensitivity and a quite accurate

20   quantitative measure, as well as to obtain a diagnosis a short time after contact between the patient and the pathogen. Nevertheless the precision and accuracy of this system is assured in a narrow quantitation range, thus forcing the operator to multiply the number of replies (typically 8) of the sample under investigation; furthermore a long time and additional costs

for the amplified product detection steps are necessary.

The first systems that assessed PCR kinetics in real time were based on an intercalating substance such as ethidium bromide. This substance binds to the polymerizing double strand DNA proportionally, enhancing its fluorescence in response to UV excitation; the fluorescence emitted from the intercalated ethidium molecules was registered by a CCD camera in a thermal cycler equipped to irradiate the samples with UV rays and plotted against the amplification cycle number (Higuchi et al., Biotechnology 10:413-417). The main limitation of this technique is that the signal is generated also from the unspecific PCR products.

Subsequently the method known as TaqMan, described in US 5210015 was introduced. This method is based on the real time detection of the fluorescence deriving from the degradation, directly dependent on the nascent PCR product, of a labeled probe specifically hybridizing to the segment to amplify, by means of the Taq polymerase enzyme. The PCR reaction mix contains a non-extendable oligonlucleotide probe, labeled with two fluorescent molecules, a reporter at the 5' end, and a quencher at the 3' end; the probe sequence must be complementary to a region of the DNA under investigation located between the two annealing sites of the oligonucleotide primers.

During the PCR amplification reaction, the Taq Polymerase enzyme specifically activated by the primers starts duplicating the DNA under investigation; when the enzyme contacts the probe annealed to the DNA, cuts it by its 5' nuclease activity, removing it and consequently separating the fluorescent molecules; the emission from the reporter fluorochrome becomes thus measurable and, each DNA molecule being accompanied by a reporter molecule release, the total fluorescence is at any time

proportional to the amplified DNA amount. The Sequence Detection System 7700 ABI PRISM (produced and distributed by Perkin Elmer) can work both as a DNA amplifier and a collector of fluorescence signals from samples during the PCR reaction. These signals are then processed

5  by a software capable of extrapolating the starting DNA amount in the analyzed samples by a standard curve built with the fluorescence signals from samples with known DNA content. It must be noted that such a system is endowed with two specificity levels: the specific annealing of the primers and the specific annealing of the probe.

10  SUMMARY OF THE INVENTION

A method generally applicable to the nucleic acid quantitation techniques based on the polymerase and 5' nuclease activity of nucleic acid polymerases, improving the efficiency of the techniques themselves, along with an enhanced sensitivity, accuracy and precision and a reduced

15  measure variability, has now been found.

The method of the invention is based on the use of a calibrator during the steps of extraction of the sample, of target nucleic acid amplification and subsequent detection with suitable probes able to differentially hybridize to the calibrator and the target sequence.

20  The method of the invention can be applied to any absolute quantitation of nucleic acids from different biological sources, for example to the quantitation of viral or bacterial pathogens in body liquids (liquor, urine, plasma, serum, synovial fluid) or to the quantitation of environmental or food contaminants.

25  DETAILED DESCRIPTION OF THE INVENTION

Nucleic acid quantitation techniques, using the polymerase and 5' nuclease activity of the nucleic acid polymerases, rely on the extraction of

nucleic acid from the sample, on the preparation of a reaction mix containing a polymerase, primers specific for the target sequence and a probe specific for a target sequence included between the regions complementary to the two primers, said probe being labeled with a

5    reporter (this reporter being preferably a fluorochrome) and a quencher, followed by determination of the signal from the reporter label released when the polymerase contacts the 5' end of the probe annealed to the target nucleic acid.

According to the method of the invention, a known amount of the

10   template nucleic acid, hereafter referred to as calibrator, is added to the sample before the extraction of the nucleic acid to be quantitatively detected (target nucleic acid). The calibrator has a sequence identical to the target nucleic acid sequence with the exception of one or more regions whose sequence is different from the corresponding regions of the target

15   nucleic acid, having with respect to the latter a randomized sequence and a similar Tm. More specifically, one of those different regions must be the region complementary to the probe, with a Tm comprised in the range of ±4°C the Tm of the target nucleic acid, preferably in the range ±2. The other different regions of the calibrator may be those annealing with the

20   primers, which have randomized sequences with respect to the target nucleic acid and a Tm comprised in the range of ±1°C the Tm of the target nucleic acid.

When this second embodiment is provided, i.e. when the calibrator regions complementary to the primers are varied with respect to the target

25   nucleic acid, in addition to the regions complementary to the probe, it is possible to extremely reduce the competition events occurring between the target template and the calibrator, and to simultaneously measure the

target template and the calibrator in a single reaction tube.

After extraction, the primers, and separately the probes derivatized with a reporter and a quencher, where the reporter can be equal or different among different probes, are added to the extracted sample-calibrator mixture. Two or more primers may be added to the reaction mixture, depending on the number of variable regions present on the calibrator annealing with the primers. Preferably, up to 3 pairs, more preferably up to two pairs of primers (forward and reverse) are used. Furthermore a thermostable polymerase with 5'-3' nuclease activity is added, thus starting the polymerase/nuclease reaction.

The reaction is carried out in a Sequence Detection System 7700 ABI PRISM that can work both as a DNA amplifier and a collector of fluorescence signals emitted from the reporter markers released upon polymerase nuclease activity. Virtually, three reactions are carried out in parallel, one of them in the presence of target nucleic acid specific probe, one in the presence of the calibrator specific probe/primers, and one in the presence of both.

The reaction in the presence of the target nucleic acid specific probe permits quantitation of the copy number of the extracted target nucleic acid ($N_o$). The reaction in the presence of the calibrator permits quantitation of the calibrator copy number recovered upon extraction ($C_o$). The reaction in the presence of both permits calculation of the total number of target templates and calibrator (T).

It is thus possible to calculate the percentage of the calibrator recovery yield R:

$$R = C_o/C,$$

from which the calibration factor (cal)

$$cal = 1/R$$

and thus the actual number of nucleic acid units in the sample before extraction are obtained:

$$N = N_0 \times Cal$$

5　　　　The relation

$$T = N_0 + C_0$$

assures that the amplification efficiency of the standard and calibrator DNA remain identical.

The calibrator non-amplification makes it possible to detect any

10　false negatives (technical errors or presence of inhibitors), which represent one of the most important drawbacks when using amplification methods in clinical diagnostics.

The reaction conditions are the same as those commonly adopted in qcPCR reactions (Petrik j. et al., J. Virol. Methods, 64:147-159, 1997).

15　The reaction conditions can be modified in order to compensate for the competition events, more exactly the primer concentration, the polymerase enzyme concentration, the annealing/extension time, or the concentration of cofactors such as $MgCl_2$ can be modified.

The target nucleic acid can be DNA or RNA, preferably DNA,

20　while primers and probes are preferably deoxyribonucleotide sequences. When the nucleic acid is RNA a previous retro-transcription step is required in order to obtain the corresponding DNA. The probes include a fluorescent reporter label and a quencher label to reduce or to avoid fluorescence from the reporter label when the probes are free in solution.

25　　　　TET (tetrachloro-6-carboxy-fluorescein), JOE (2,7-dimethoxy-4,5-dichloro-6-carboxyfluorescein), HEX (hexachloro-6-carboxy-fluorescein) are examples of reporter, preferably TAMRA (6-carboxy-tetramethyl-

rhodamine) and FAM (6-carboxy-fluorescein) are used as quencher and reporter, respectively.

Preferably the 5' end of said probes is in the range of 1 to 30 nucleotides from the 3' end of the forward primer, i.e. at a distance to permit the reporter label release in the absence of nucleic acid polymerization. Preferably, the probes have a blocked 3' end in order to prevent the extension by polymerase, have a Tm higher than the primer Tm, and comprise 18 to 30 nucleotides.

The nucleic acid polymerase is a thermostable polymerase with 5'-3' nuclease activity, preferably a DNA polymerase, and more preferably a DNA polymerase derived from the Thermus species.

A great advantage of the described method is represented by the possibility to detect samples containing inhibitors and to mathematically characterize the yield of genetic material extraction. A further advantage is represented by the possibility of simultaneously measuring the calibrator and the target nucleic acid in the same reaction tube. The possibility of detecting total inhibitors of amplification reaction from the samples allows the elimination of false negatives often occurring with known techniques. Moreover, the calibration does not necessitate further standardization which is conversely required, for example, by the TaqMan technique (see Chatellard P. et al., J. Virol. Methods, 71:137-146, 1998).

The present invention also provides a kit to perform the above described method, including, depending on the target nucleic acid, a suitable calibrator, a probe specific for the target nucleic acid, two or more primers and a nucleic acid polymerase.

According to a preferred embodiment, the method of the invention is employed to quantitatively detect the genomic nucleic acid of the HHV-

6, HHV-7, HHV-8, and HIV viruses, in a sample.

Particularly, in the case of HHV-6, the assay is divided into two steps: in the first step gene extraction is performed by a method based on the standard lysis-purification protocol by phenol-chloroform; in the second step the amplification reaction is carried out with specific primers and probes, selected by the "Primer Express" software (Perkin Elmer).

The primer and probe have been designed to amplify both type A and type B HHV-6 strains with the same efficiency. This feature is responsible for very high diagnostic sensitivity.

The calibration according to the method of the invention relies on adding to the sample, before DNA extraction, a known amount of a template DNA amplifiable with the same kinetic properties as the HHV-6 amplicon, but at the same time clearly distinguishable from it. A DNA fragment identical to that amplified by the HHV-6 primers, apart from the region complementary to the probe that has been modified so as to preserve the same nucleotide composition but with a random sequence, and with the same melting temperature (Tm), is thus cloned; the obtained plasmid, termed "calibrator", is amplified by the same primers and with the same kinetic as the standard plasmid, but it is revealed by the 7700 software only if the PCR mix contains a probe with a sequence complementary to the random sequence.

The calibrator plasmid is expanded and accurately quantitated by the spectrophotometer so as to add an exact amount of it to the samples to be extracted. Upon DNA extraction, samples thus contain a certain number of HHV-6 genomes and calibrator plasmid copies, dependent on the total yield of such an extraction; the HHV-6 DNA quantitation is thus possible, assuming such a yield to be identical for both the molecular

species.

The reaction specific conditions are indicated in further detail in the example section.

To compensate for competition events, the reaction conditions were modified as follow: the primer concentration was elevated ten-fold, enzyme concentration was doubled, the amplification annealing/extension was increased by 8 seconds per cycle starting from the initial 60 seconds. However the competition events between templates narrowed the range of absolute quantitation (calibrated) from 7 to 5 order of magnitude, 2 above and 2 under the value of the calibrator input, while the relative quantitation range (non calibrated) and the ability to detect the experimental false negatives are unchanged.

According to an alternative embodiment, the original calibrator sequence has been further randomized in the two primers coding regions maintaining the theoretical Tm of the two original primers (as calculated by the specific software Primer Express PE foster city CA). The relevant sequences of the new calibrator molecules are reported in Table 2 of the examples. The target DNA molecule and the calibrator were amplified with the same kinetics, as evidenced by the following equations:

$y=37.804 + -3.4402 \times LOG(x)$ $R = 1.000$ for the standard template amplification, and $y= 38.543 + -3.568 \times LOG(x)$ $R = 0.998$ for the calibrator template amplification.

The two molecules added in the same tube were correctly co-amplified, using standard PCR reactions, for more than 7 order of magnitude with no necessity to compensate for competitive events.

In order to carry out the simultaneous detection and quantification of target DNA and calibrator in a single tube the calibrator was derivatized at

the 5'end with VIC (Pe Biosystem), a fluorescent molecule having an emission spectrum different from the one used for the target DNA molecule detection.

To eliminate the interference generated by the partial overlapping of the emission spectra of the two dyes, the calibrator PCR conditions were modified by reducing the primers and probe concentrations (final concentration 50nM for both). The reduction of the emission signal of VIC reporter was achieved without modification of the Ct (Cycle threshold) value, thus allowing a reproducible quantitation of the calibrator itself.

The spectral interference was completely avoided by adding the calibrator in a fixed concentration one log higher than the maximal amount of standard used in the reference curve (i.e. 10,000,000 copies of calibrator for a standard curve in which the highest concentration of standard was 1,000,000 copies reaction).

The following examples illustrate the invention in further detail.

EXAMPLES

Example 1

Selection of the HHV-6, HHV-7, HHV-8, HIV, 35s CAMV and Mycobacterial sequences.

The U67 HHV-6 region (A variant, GeneBank Accession N°. X83413) and the 26 HHV-8 orf region (Chang et al., Science 266, 1865-1869, 1994) the HHV-7 region (Gene Bank AF037218), 35sCAMV (Gene Bank AF140604), RegX-SenX (Gene Bank MTY 13628) and 156110 (Gene Bank X17848), and the HIV region mapping between the LTR and gag region from nucleotide 684 to 810 using the sequence HXB2CG-Accession number K03455 (Gene Bank) are reported in Table 1 (primers

and probe of the target nucleic acid and calibrator probe). The HHV-6

sequences (primers and probe for the target, calibrator's primers and

probe) are reported in Table 2.

The probe sequences of the calibrators (HHV-7, HHV-8, HIV-1,

5   CAMV, Myc. T.) and the calibrator's primers (HHV-6) were designed

randomizing the probe region of the standard, while maintaining:

1. the same base composition (G+C/A+T) of the standard

2. an identical Tm (calculated by Perkin Elmer software)

3. an identical length (in order to have the same amplification efficiency)

10  4. and being characterized by an absolute absence of homology with the

standard (target) in order to avoid cross-hybridization and

interferences.

Table 1

|  | Primers | | Probes | |
|---|---|---|---|---|
| HHV-7 | Forward | 5' AGCGGGTACCTGTAAAATCATCCA3' | Standard | 5' ACCAGTGAGAACATCGCTCTAACTGGATCA 3' |
|  | Reverse | 5' AACAGAAACGCCACCTCGAT 3' | Calibrator | 5' TAAGCCCTGACCGCACGGGTATAAATACTAA 3' |
| HHV-8 | Forward | 5'GTCCAGACGATATGTGCGC3' | Standard | 5'CATTGGTGGTGTATATAGATCAAGTTCCGCCA3' |
|  | Reverse | 5'ACTCCAAAATATCGGGCCGG3' | Calibrator | 5'ACTATTCCATGCGGAATTCGAGCATAGTTG3' |

(continued)

Table 1 (continued)

| | Primers | | Probes | |
|---|---|---|---|---|
| HIV-1 | Forward | 5' TACTGACGCTCTCGCACC 3' | Standard | 5' ATCTCTCTCCTTCTAGCCTCCGCTAGTCAA 3' |
| | Reverse | 5' TCTCGACGCAGGACTCG 3' | Calibrator | 5' ACTCTCAGCGGGCATTCTCCTCACTTCTACT 3' |
| CAMV | Primers | | Probes | |
| | Forward | 5' GTCTTGCGAAGGATAGTGGGA 3' | Standard | 5' TGCGTCATCCCTTACGTCAGTGGAGAT 3' |
| | Reverse | 5' CACGTCTTCAAAGCAAGTGGA 3' | Calibrator | 5' ATCGCTACATGCTAGGCATCTGTGTGC 3' |

(continued)

Table 1 (continued)

|  | Primers |  | Probes |  |
|---|---|---|---|---|
| Myc. T. 1 | Forward | 5' AGGAGGAGTGGGCGCTGATG 3' | Standard | 5' ACGAGGAGTCGCTGGCCGATCC 3' |
|  | Reverse | 5' ACTCGGGCGAGAGCTGCC 3' | Calibrator | 5' TCCAGCGTCAGGCGTAGGCAGC 3' |
| Myc. T. 2 | Forward | 5' AGGCGAACCCTGCCCAG 3' | Standard | 5' TCGACACATAGGTGAGGTCTGCTACCCACA 3' |
|  | Reverse | 5' GATCGCTGATCCGGCCA 3' | Calibrator | 5' ACTACGACTACGGCTGCGATCGACATCGAT 3' |

Table 2

| | Primers | | Probes | |
|---|---|---|---|---|
| HHV-6 | Forward | 5' CAAAGCCCAAATTATCCAGAGCG 3' | Standard | 5' CACCAGACGTCACACCCGAAGGAAT 3' |
| | Reverse | 5' CGCTAGGTTGAGGATGATCGA 3' | Calibrator | 5' TACGCAACGCCAACAGACCTAGCGA 3' |
| | Calibrator | | | |
| | Primer forward | 5' CCGGAAACCGAACATTACTGAA 3' | Probe | 5' TACGCAACGCCAACAGACCTAGCGA 3' |
| | Primer reverse | 5' TTACGTGAGGATGATCGAGGC 3' | | |

Example 2

HHV-6 Standard (target nucleic acid) and Calibrator cloning and preparation.

The fragments used for the standard and calibrator DNA
5   construction in the HHV-6 virus detection system are schematically represented in Figure 1 (1-A and 1-B respectively).

The Standard fragment sequence was obtained by amplification of the viral DNA from HHV-6 GS strain and subsequent cloning into pCRII plasmid vector (Invitrogen). The calibrator fragment (133 bp) was
10   chemically synthesized by an Oligosynthetizer (Perkin Elmer), and then cloned in the same vector as above.

After cloning, both fragments were completely sequenced in order to identify: i) the identity (co-linearity) of the standard fragment with the original viral DNA, ii) the identity of the calibrator fragment with the
15   artificially designed sequence.

As shown in Figure 1, the arrows, oriented in the transcription direction, indicate the oligonucleotide sequence employed as primers. The dotted line identifies in both constructs the regions of 25 nucleotide used as the probes (lowercase) differentiating the two constructs, otherwise
20   identical in the remaining 108 nucleotides. These regions, even though they have the same base composition and a very similar Tm, were designed in such a way as to function as a heterologous system, allowing avoidance or minimization of the cross-hybridization events between the probes employed in the specific fluorimetric detection and the standard
25   and calibrator fragments.

Example 3

HHV-6 calibrator/standard system validation

Absence of cross-hybridization

We thus experimentally verified the absence of spurious signals

5    from cross-hybridization. Increasing concentrations of the standard and

calibrator fragment (from 101 to 106 plasmid copies per PCR reaction)

were measured using the homologue probe (standard probe for the

standard DNA, calibrator probe for the calibrator DNA) or the

heterologous probe (standard probe for the calibrator DNA, calibrator

10   probe for the standard DNA). Figure 2B shows the detection of the

various template amounts employing the probe homologous to the

fragment to measure, where: a) indicates the standard amplification curve

and, b) the calibrator curve. Detection takes place for both constructs with

overlapping kinetics (curves 1-5, a, b) furthermore indicating that the

15   template amplification is proportional to the measured fluorescence

signal. The use of heterologous probe (Fig. 2A) for both templates does

not generate a signal appreciably higher than the system background

noise.

Co-linearity

20   Amplification co-linearity of the two templates was measured by

comparing the two regression line equations generated from the values

obtained as threshold cycles as a function of the increasing copy number

of the employed template.

The resulting equations are:

25   $y=37.804 + -3.4402 \ X \ LOG(x) \ R = 1.000$ for the standard template

amplification

$y= 38.543 + -3.568 \ X \ LOG(x) \ R = 0.998$ for the calibrator template

amplification.

The slope ratio of the two lines is 1.017 thus indicating that the two systems are perfectly overlapping both as amplification efficiency and as fluorimetric detection dynamics.

5    Calibration range

Amplification of the two templates in the same PCR reaction causes an appreciable modification of the amplification curve detected by the system (Fig. 3A). In fact it is possible that for increasing copy amounts, i.e. 500 calibrator copies in unique dose co-amplified in the presence of 0,

10   500, 5,000, 50,000, 500,000 standard copies (from 1a-1e respectively), the fluorescent signal is changed both in the accumulation kinetic and in the final amount of the released product. At the threshold cycle (A' insert), standard template concentrations equivalent to or higher by a Log (A' insert − 1a-1c curves) do not influence the accuracy of the calibrator

15   quantitation. For higher concentrations (1d, 1e curves) the quantitation is partially (marked delay of the threshold cycle, 1d) or completely impaired (1e). The optimization of the PCR conditions, and particularly the combined actions of primer concentration increase (from 300 nM to 3 μM), doubling the enzyme concentration (from 0.625 to 1.25 AmpliTaq

20   Gold units), and the increase in length of every PCR cycle (8 sec. increment per cycle during the annealing and extension steps), cause an improvement of the amplified product accumulation kinetic and of the final yield of the fluorescence signal (Fig. B, curves 1a-1e). At the threshold cycle (B' insert), standard template concentrations up to 2 Log

25   (50,000 copies) higher than the calibrator input, do not modify its quantitation (B' curves 1e-1d). For higher concentrations (500,000 copies) the fluorimetric signal from the calibrator probe is measurable, although

the lack of signal exponential increase does not allow maintenance of an accurate measure of the calibrator (B' curve 1e).

In opposite conditions (Fig. 4A), i. e. with excess of calibrator up to 2 Log concentration with respect to the standard, (e. g. 500 copies of calibrator vs. 5 copies of standard), the analysis of the reaction kinetics is as above. In particular, in optimized conditions, the quantitation at the threshold cycle (A' insert; "a" indicates the amplification curve of the standard in the absence of the calibrator, "b" the curve measured in the presence of the calibrator), in this case of the standard, is not modified (A' curves 1a-1b: 100 copies of standard and 25 copies of standard concentration, 3a-b:5 copies of standard concentration).

By means of this optimization it can thus be obtained an accurate quantitation of a template whose amount is unknown, with the following practical advantages:

1) Absolute control (both qualitative and quantitative) of the whole process of sample purification and amplification with a dynamic range of at least 5 Log (e. g. 5 to 50,000 copies per reaction);

2) Quantitative control of purification and amplification process with a dynamic range of at least 7 logarithms (false negatives due to technical error or to the presence of contaminants inhibiting the PCR reaction).

3) Eliminating the unknown sample serial dilution;

4) Inserting only one known dose of the calibrator (e. g. 500 copies).